WEST Search History

DATE: Tuesday, May 13, 2003

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=OR			
L6	L5 and reduced adj4 immunogen$4	12	L6
L5	Diver$8 DNA adj6 library adj6 variant	347294	L5
L4	L3 and competitive adj6 assay	31	L4
L3	L2 and red$6 adj4 immunog$8	177	L3
L2	L1 and diver$8	5624	L2
L1	DNA adj4 library	12728	L1

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=> s diver?(5w)(DNA or gene)(5w)lib?
L1 16 DIVER?(5W)(DNA OR GENE)(5W) LIB?

=> d l1 1-16 so au py ab

L1 ANSWER 1 OF 16 CA COPYRIGHT 2003 ACS
SO PCT Int. Appl., 66 pp.
CODEN: PIXXD2
IN Ashkar, Samy
PY 2002
AB The present invention is generally in the field of high throughput peptide screening. A minicell display method has been developed which has significant advantages for screening peptide libraries for candidate that can bind and effectively modulate a particular biol. process. Minicells are small, anucleate cells resulting from aberrant cell divisions at the polar ends of bacteria. However, the minicells are large enough to harbor several plasmids. The method has increased versatility in generating unique sequences to screen as well as increasing the size of the peptides to be screened. These methods include selecting new and unique target interacting peptides from minicell display libraries of random oligonucleotides that are expressed as gene fusions to a protein. The plasmid or expression vector encoded oligonucleotide fusion or gene fusion product is preferably localized to the minicell outer membrane forming what is referred to as a "display minicell". The method consists of first constructing a library wherein the library consists of a replicable expression vector includes an inducible transcriptional regulatory element operably linked to a gene fusion, where the gene fusion includes: (i) a first gene encoding at least a portion of a bacterial outer membrane protein (such as 17-K antigen of Rickettsia rickettsii); and (ii) a second gene or oligonucleotide encoding a potential "substrate" peptide interacting with a target mol. The 3' end of the first gene is linked to the 5' end of the second gene or oligonucleotide, thereby forming a chimeric gene. The linkage between the first and second gene may be direct, or indirect via a linker mol. or oligonucleotide. In vivo mutagenesis, at the level of protein synthesis, as well as DNA replication, increases diversification of the library to be screened and therefore substantially increases the no. of potential peptides that can modulate a particular biol. response or mechanism.

L1 ANSWER 2 OF 16 CA COPYRIGHT 2003 ACS
SO Asahi Garasu Zaidan Josei Kenkyu Seika Hokoku [online computer file] (2001) No pp. given
CODEN: AGSHEN; ISSN: 0919-9179
URL: http://www.af-info.or.jp/jpn/subsidy/report2/2001/body/01A-C16-P080.TXT
AU Ebara, Yasuhito
PY 2001
AB Nonnatural nucleotide modified by amino acid, glucose and galactose was synthesized to increase functional **diversity** of **DNA library**. These compds. were incorporated in a DNA double strand using Klenow Fragment as well as dTTP. These functional group could be ordered sequentially on a DNA double strand at intervals of few angstroms according to the designed template sequence within a few hours. This method must be useful to constructing nonnatural DNA library or designed supramol. structures.

L1 ANSWER 3 OF 16 CA COPYRIGHT 2003 ACS
SO Animal Biotechnology (2002), 13(1), 163-172
CODEN: ANBTEN; ISSN: 1049-5398
AU Band, Mark R.; Olmstead, Colleen; Everts, Robin E.; Liu, Zonglin L.; Lewin, Harris A.
PY 2002
AB A cDNA microarray representing .apprx.3800 cattle genes was created for functional genomic studies. The array elements were selected from >7000 cDNA clones identified in a large-scale expressed sequence tag (EST) project that utilized spleen and normalized and subtracted placenta cDNA libraries. Sequence similarity searches of the 3820 ESTs represented on the array using BLASTN identified 3290 (86.1%) as putative human orthologs, with the remainder consisting of "novel" genes or highly divergent orthologs. Expts. were conducted with a prototype 768 gene microarray created from spleen cDNAs and with the 3800 gene array that included genes from spleen and placenta. The 768 gene array was used to profile RNA transcripts expressed by adult and fetal spleen. The 3800 gene array was used to profile transcripts expressed by adult brain and placenta. Microarray anal. of RNA extd. from fetal and adult spleen identified 29 genes that were differentially expressed .gtoreq.2-fold. Transcriptional differences of two of these genes, IGJ and CTSS, were confirmed using TaqMan technol. The comparison of brain and placenta revealed 400 genes expressed at higher levels in brain and 72 genes expressed at higher levels in placenta. These results demonstrate the potential power of microarrays for understanding the mol. mechanisms of cattle development, disease resistance, nutrition, fertility, and prodn. traits. Sequence data for all ESTs used for construction of the arrays and annotations are available in GenBank and at http://keck1.biotec.uiuc.edu/cattle/cattle_project.htm. [This abstr. record is one of five records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L1 ANSWER 4 OF 16 CA COPYRIGHT 2003 ACS
SO Animal Biotechnology (2002), 13(1), 163-172
CODEN: ANBTEN; ISSN: 1049-5398
AU Band, Mark R.; Olmstead, Colleen; Everts, Robin E.; Liu, Zonglin L.; Lewin, Harris A.
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system constraints.].

L1 ANSWER 5 OF 16 CA COPYRIGHT 2003 ACS
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L1 ANSWER 6 OF 16 CA COPYRIGHT 2003 ACS
SO Animal Biotechnology (2002), 13(1), 163-172
CODEN: ANBTEN; ISSN: 1049-5398
AU Band, Mark R.; Olmstead, Colleen; Everts, Robin E.; Liu, Zonglin L.; Lewin, Harris A.
PY 2002
AB A cDNA microarray representing .apprx.3800 cattle genes was created for functional genomic studies. The array elements were selected from >7000 cDNA clones identified in a large-scale expressed sequence tag (EST) project that utilized spleen and normalized and subtracted placenta cDNA libraries. Sequence similarity searches of the 3820 ESTs represented on the array using BLASTN identified 3290 (86.1%) as putative human orthologs, with the remainder consisting of "novel" genes or highly divergent orthologs. Expts. were conducted with a prototype 768 gene microarray created from spleen cDNAs and with the 3800 gene array that included genes from spleen and placenta. The 768 gene array was used to profile RNA transcripts expressed by adult and fetal spleen. The 3800 gene array was used to profile transcripts expressed by adult brain and placenta. Microarray anal. of RNA extd. from fetal and adult spleen identified 29 genes that were differentially expressed .gtoreq.2-fold. Transcriptional differences of two of these genes, IGJ and CTSS, were confirmed using TaqMan technol. The comparison of brain and placenta revealed 400 genes expressed at higher levels in brain and 72 genes expressed at higher levels in placenta. These results demonstrate the potential power of microarrays for understanding the mol. mechanisms of cattle development, disease resistance, nutrition, fertility, and prodn. traits. Sequence data for all ESTs used for construction of the arrays and annotations are available in GenBank and at http://keck1.biotec.uiuc.edu/cattle/cattle_project.htm. [This abstr.

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L1 ANSWER 7 OF 16 CA COPYRIGHT 2003 ACS
SO Animal Biotechnology (2002), 13(1), 163-172
CODEN: ANBTEN; ISSN: 1049-5398
AU Band, Mark R.; Olmstead, Colleen; Everts, Robin E.; Liu, Zonglin L.; Lewin, Harris A.
PY 2002
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L1 ANSWER 8 OF 16 CA COPYRIGHT 2003 ACS
SO Mammalian Genome (2002), 13(7), 373-379
CODEN: MAMGEC; ISSN: 0938-8990
AU Sonstegard, Tad S.; Capuco, Anthony V.; White, Joseph; Van Tassell, Curtis P.; Connor, Erin E.; Cho, Jennifer; Sultana, Razvan; Shade, Larry; Wray, James E.; Wells, Kevin D.; Quackenbush, John
PY 2002
AB Functional genomic studies of the mammary gland require an appropriate collection of cDNA sequences to assess gene expression patterns from the different developmental and operational states of underlying cell types. To better capture the range of gene expression, a normalized cDNA library was constructed from pooled bovine mammary tissues, and 23,202 expressed sequence tags (EST) were produced and deposited into GenBank. Assembly of these EST with sequences in the Bos taurus Gene Index (BtGI) helped to form 5751 of the current 23,883 tentative consensus (TC) sequences. The majority (87%) of these 5751 assemblies contained only one to three mammary-derived EST. In contrast, 18% of the mammary EST assembled with TC sequences corresponding to 12 genes. These results suggest library normalization was only partially effective, because the redn. in EST for genes abundantly transcribed during lactation could be attributed to pooling. For better assessment of novel content in the mammary library and to add to existing annotation of all bovine sequence elements, gene ontol. assignments, and comparative sequence analyses against human genome sequence, human and rodent gene indexes, and an index of orthologous alignments of genes across eukaryotes (TOGA) were performed, and results were added to existing BtGI annotation. Over 35,000 of the bovine elements significantly matched human genome sequence, and the positions of

some alignments (3%) were unique relative to those using human expressed sequences. Because 3445 TC sequences had no significant match with any data set, mammary-derived cDNA clones representing 23 of these elements were analyzed further for expression and novelty. Only one clone met criteria suggesting the corresponding gene was a divergent ortholog or expressed sequence unique to cattle. These results demonstrate that bovine sequence expression data serve as a resource for characterizing mammalian transcriptomes and identifying those genes potentially unique to ruminants. [This abstr. record is one of six records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L1 ANSWER 9 OF 16 CA COPYRIGHT 2003 ACS
SO PCT Int. Appl., 76 pp.
CODEN: PIXXD2
IN Carlsson, Roland; Furebring, Christina; Malmborg Hager, Ann-Christin; Borrebaeck, Carl
PY 2002
2002
2003
2002
2002
AB A method of generating a diverse sequence population from a starting DNA sequence using a single-stranded DNA intermediate is described. The two strands are sepd. and are sep. digested with a progressive exonuclease to create a library of fragments. The two sets of fragments are mixed, hybridized and ligated to create a diversified library of sequences. Optionally, the ligation mixt. may amplified using primers derived from areas of interest in the gene, such as those encoding specific protein motifs. Preferably, the exonuclease is BAL 31. The library can then be screened for genes conferring a desired phenotype. Optimization expts. showing the efficiency of the method in generation of diversity are reported. Expts. demonstrating that the use of exonucleases gives greater diversity in the library than the use of endonucleases are reported.

L1 ANSWER 10 OF 16 CA COPYRIGHT 2003 ACS
SO PCT Int. Appl., 89 pp.
CODEN: PIXXD2
IN Short, Jay M.
PY 2001
2002
2002
2001
2002
AB Provided is a method of obtaining a nucleic acid profile of a sample. The method includes creating a DNA library from a plurality of nucleic acid sequences of a mixed population of organisms and sequencing at least one clone in the DNA library. The microorganisms are extremophiles, including thermophiles, hyperthermophiles, psychrophiles, halophiles, acidophiles, barophiles and psychrotrophs. The sequence is compared to a database, such as GenBank, PFAM and ProDom, and identifying sequences in the database which have homol. to a clone in the library thereby obtaining a nucleic acid profile of the mixed population of organisms. The algorithm for homol. search is selected from Smith-Waterman, Needleman-Wunsch, BLAST, FASTA, BLITZ and PSI-BLAST.

L1 ANSWER 11 OF 16 CA COPYRIGHT 2003 ACS
SO Current Opinion in Biotechnology (2001), 12(4), 340-347
CODEN: CUOBE3; ISSN: 0958-1669
AU Pelletier, J.; Sidhu, S.
PY 2001
AB A review with 68 refs. Extremely **diverse**, **DNA**-encoded **libraries** of peptides and proteins have been constructed that include a linkage between each polypeptide and the encoding DNA. Library

members can be selected by virtue of a particular binding specificity, and their protein sequence can be deduced from the sequence of the cognate DNA. Such combinatorial biol. methods have proven invaluable in both identifying natural protein-protein interactions and also in mapping the specificities and energetics of these interactions in fine detail.

L1 ANSWER 12 OF 16 CA COPYRIGHT 2003 ACS
SO Genome Research (2000), 10(8), 1103-1107
CODEN: GEREFS; ISSN: 1088-9051
AU Porcel, Betina M.; Tran, Anh-Nhi; Tammi, Martti; Nyarady, Zoltan; Rydaker, Maria; Urmenyi, Turan P.; Rondinelli, Edson; Pettersson, Ulf; Andersson, Bjorn; Aslund, Lena
PY 2000
AB A survey of the active genes in the important human pathogen Trypanosoma cruzi was performed by analyzing 5013 expressed sequence tags (ESTs) generated from a normalized epimastigote cDNA library. Clustering of all sequences resulted in 771 clusters, comprising 54% of the ESTs. In total, the ESTs corresponded to 3054 transcripts that might represent one-fourth of the total gene repertoire in T. cruzi. About 33% of the T. cruzi transcripts showed similarity to sequences in the public databases, and a large no. of hitherto undiscovered genes predicted to be involved in transcription, cell cycle control, cell division, signal transduction, secretion, and metab. were identified. More than 140 full-length gene sequences were derived from the ESTs. Comparisons with all open reading frames in yeast and in Caenorhabditis elegans showed that only 12% of the T. cruzi transcripts were shared among diverse eukaryotic organisms. Comparison with other kinetoplastid sequences identified 237 orthologous genes that are shared between these evolutionarily divergent organisms. The generated data are a useful resource for further studies of the biol. of the parasite and for development of new means to combat Chagas' disease.

L1 ANSWER 13 OF 16 CA COPYRIGHT 2003 ACS
SO PCT Int. Appl., 103 pp.
CODEN: PIXXD2
IN Catcheside, David E.
PY 1999
2001
1999
2002
AB Claimed is a method of generating a **diverse** heterologous **DNA** sequence **library** in a haploid fungus which is capable of becoming diploid by configuring the recombinant DNA to include a recombination hotspot functionally coupled to the heterologous DNA. The fungi used include Neurospora crassa, Schizosaccharomyces pombe, and Saccharomyces cerevisiae. The process of recombination generates new versions of the foreign sequences by recombining their differences in new combinations. Errors in recombination generate addnl. sequence diversity. An auxotrophic mutation may be used as a forcing marker.

L1 ANSWER 14 OF 16 CA COPYRIGHT 2003 ACS
SO Applied and Environmental Microbiology (1996), 62(4), 1171-7
CODEN: AEMIDF; ISSN: 0099-2240
AU Gordon, D. A.; Giovannoni, S. J.
PY 1996
AB A gene lineage (SAR406) related to Chlorobium and Fibrobacter species was found in 16S rRNA gene clone libraries prepd. from samples from two oceans. The clone libraries were constructed from total picoplankton genomic DNA to assess bacterial diversity in the lower surface layer. The samples were collected by filtration from a depth of 80 m at a site in the western Sargasso Sea and from a depth of 120 m at a site in the Pacific Ocean, approx. 70 km from the Oregon coast. The PCR and primers which amplified nearly full-length 16S rRNA genes were used to prep. the clone libraries. Among the **diverse gene** clones in these

libraries were two related clones (SAR406 and OCS307) which could not be assigned to any of the major bacterial phyla. Phylogenetic analyses demonstrated that these genes were distant relatives of the genus Fibrobacter and the green sulfur bacterial phylum, which includes the genus Chlorobium. The inclusion of SAR406 in phylogenetic trees inferred by several methods resulted in support from bootstrap replicates for the conclusion that Fibrobacter and Chlorobium species and SAR406 are a monophyletic group. An oligonucleotide probe that selectively hybridized to clone SAR406 was used to examine the distribution of this gene lineage in vertical profiles from the Atlantic and Pacific Oceans and in monthly time series at 0 and 200 m in the Atlantic Ocean. During stratified periods, the genes were most abundant slightly below the deep chlorophyll layer. Seasonal changes in the surface abundance of SAR406 rDNA were highly correlated with chlorophyll a levels (r = 0.75).

L1 ANSWER 15 OF 16 MEDLINE
SO CURRENT OPINION IN BIOTECHNOLOGY, (2001 Aug) 12 (4) 340-7. Ref: 68
Journal code: 9100492. ISSN: 0958-1669.
AU Pelletier J; Sidhu S
PY 2001
AB Extremely **diverse**, **DNA**-encoded **libraries** of peptides and proteins have been constructed that include a linkage between each polypeptide and the encoding DNA. Library members can be selected by virtue of a particular binding specificity, and their protein sequence can be deduced from the sequence of the cognate DNA. Such combinatorial biology methods have proven invaluable in both identifying natural protein-protein interactions and also in mapping the specificities and energetics of these interactions in fine detail.

L1 ANSWER 16 OF 16 MEDLINE
SO APPLIED AND ENVIRONMENTAL MICROBIOLOGY, (1996 Apr) 62 (4) 1171-7.
Journal code: 7605801. ISSN: 0099-2240.
AU Gordon D A; Giovannoni S J
PY 1996
AB A gene lineage (SAR406) related to Chlorobium and Fibrobacter species was found in 16S rRNA gene clone libraries prepared from samples from two oceans. The clone libraries were constructed from total picoplankton genomic DNA to assess bacterial diversity in the lower surface layer. The samples were collected by filtration from a depth of 80 m at a site in the western Sargasso Sea and from a depth of 120 m at a site in the Pacific Ocean, approximately 70 km from the Oregon coast. The PCR and primers which amplified nearly full-length 16S rRNA genes were used to prepare the clone libraries. Among the **diverse gene** clones in these **libraries** were two related clones (SAR406 and OCS307) which could not be assigned to any of the major bacterial phyla. Phylogenetic analyses demonstrated that these genes were distant relatives of the genus Fibrobacter and the green sulfur bacterial phylum, which includes the genus Chlorobium. The inclusion of SAR406 in phylogenetic trees inferred by several methods resulted in support from bootstrap replicates for the conclusion that Fibrobacter and Chlorobium species and SAR406 are a monophyletic group. An oligonucleotide probe that selectively hybridized to clone SAR406 was used to examine the distribution of this gene lineage in vertical profiles from the Atlantic and Pacific Oceans and in monthly time series at 0 and 200 m in the Atlantic Ocean. During stratified periods, the genes were most abundant slightly below the deep chlorophyll layer. Seasonal changes in the surface abundance of SAR406 rDNA were highly correlated with chlorophyll a levels (r = 0.75).

=> s library(5w)(genes or DNA)(5w)diver?(5w)antigen
L2 0 LIBRARY(5W)(GENES OR DNA)(5W) DIVER?(5W) ANTIGEN

=> s library(5w)(genes or DNA)(5w)diver?(5w)(protein(2w)variant or enzyme)

L3 0 LIBRARY(5W)(GENES OR DNA)(5W) DIVER?(5W)(PROTEIN(2W) VARIANT OR ENZYME)

=> s library(5w)(genes or DNA)(5w)(protein(2w)variant or enzyme)
L4 10 LIBRARY(5W)(GENES OR DNA)(5W)(PROTEIN(2W) VARIANT OR ENZYME)

=> d l4 1-10 ab so py

L4 ANSWER 1 OF 10 CA COPYRIGHT 2003 ACS
AB The invention relates to a method for producing novel modular enzyme systems by genetic engineering, which is characterized by a cyclic in vitro gene synthesis and which allows a specific recombination of the individual, gene-encoded modular components to novel enzyme systems. Examples of such modular enzyme systems are the non-ribosomal peptide synthetases (NRPS) or polyketide synthases (PKS) of type 1, that is the amino acid sequence of such an enzyme is characterized by being composed of a repetitive sequence of identical sequence sections or sequence sections that are very similar to one another. Every single repetitive sequence is referred to as a module and every module allows the enzymic incorporation of a specific substrate into the substance synthesized by the enzyme. The products synthesized by the NRPS and PKS enzymes are often highly valuable as pharmaceuticals, such as the penicillins, vancomycins or erythromycins. The inventive method allows for an effective prodn. of novel genes for modular enzymes, and the gene expression of said novel genes allows for the prodn. of novel substances. Thus, shuttle vectors contg. a multiple cloning site contg. 3 unique restriction sites R1, R2, and R3 are created. A **library** of R1-R3-flanked **DNA** fragments encoding **enzyme** modules is also prepd. These modules contain a third restriction site (R2) at the terminus of the module-encoding region. Ends created by cleavage at R1 and R2 are compatible. Chimeric genes are created by inserting an R1-R3-flanked DNA fragment into R1- and R3-digested vector followed by ligation, digestion with R2-cleaving restriction enzyme, and insertion of another R1-R3-flanked DNA, etc.
SO PCT Int. Appl., 83 pp.
CODEN: PIXXD2
PY 2001
2002
2003

L4 ANSWER 2 OF 10 CA COPYRIGHT 2003 ACS
AB Botrytis cinerea is a widespread pathogen producing infections on more than 200 hosts. Hosts attack can occur before harvesting or later during transport or storage. And B. elliptica causal agent of leaf blight, inflicts serious losses cut flowers of lily in Taiwan. However, B. cinerea and B. elliptica have become one of the most important threats to the prodn., import and export of cut flowers and some important crops. However, detection of the fungus at the latent stage before packing for transmitting is difficult because time consuming and tedious by classical methods. In this study we describe the development of DNA probe and polymerase chain reaction anal. to detection of B. cinerea and B. elliptica. A genomic **library** of mitochondrial **DNA**, digested with EcoRI restriction **enzyme** from isolates of WFFr103 EPL803 of B. cinerea and B. elliptica was constructed in the vector of pBluescript (SK+), and transformed into E. coli DH5 .alpha.. Randomly selected recombinant clones designated as pBE83-8 (0.9 kb) - pBE83-4B (1.2 kb) - pBE83-7 (1.1 kb) - pBC26-9 (1.2 kb) - pBC29-9 (0.7 kb) and pBC29-2 (1.2 kb) were nonradioactive labeled with NEBlot-Phototope. The sensitivity of DNA probe Be 83-8(0.9 kb) is highest up to 10-5 .mu.g among all DNA probes from dot-blot hybridization analyses with total DNA of B. cinerea and B. elliptica. But the DNA probe of Be 83-4B(1.2 kb) hybridized with all isolates of B. cinerea and B. elliptica. According to RAPD band patterns analyses with primer OPB-17 to amplify DNA of B. cinerea and B.elliptica have the 300 bp - 600 bp and 800 bp fragments in

amplified DNA after gel electrophoresis. These 300 bp - 600 bp and 800 bp fragments transformant clones were prepd. for DNA probes, as pBCE30 - pBCE60 and pBCE80. And the high specificity of DNA probes of pBCE30 - pBCE60 and pBCE80 were proved with Southern hybridization with all isolates of B. cinerea and B. elliptica. For sets of primers of PB30-1R/PB30-1F - PB60-1R/PB60-1F and PB80-1F/PB80-1R were developed from the nucleotide sequences analyzing of insert DNAs in pBCE30 - pBCE60 and pBCE80, resp., using total DNAs of B. cinerea - B. elliptica and another check fungus isolates as templates in PCR assay. The PB80-1F/PB80-1R primers set specifically amplified 890 bp DNA fragments from DNA of B. cinerea, and amplified 381 bp DNA fragments from DNA of B. elliptica but not DNA from any another check isolates as Sclerotium rolfsii and Mucor sp. Using of this highly specific and reliable detection could prove valuable for regulatory, epidemiol. and ecol. studies.

SO Zhiwu Bingli Xuehuikan (1998), 7(4), 177-188
CODEN: ZBXUFM; ISSN: 1021-9544

PY 1998

L4 ANSWER 3 OF 10 CA COPYRIGHT 2003 ACS

AB Disclosed is a process for obtaining an enzyme having a specified enzyme activity derived from a heterogeneous DNA population by screening, for the specified enzyme activity, a library of clones contg. DNA from the heterogeneous DNA population which have been exposed to directed mutagenesis towards prodn. of the specified enzyme activity. Also disclosed is a process for obtaining an enzyme having a specified enzyme activity by screening, for the specified enzyme activity, a library of clones contg. DNA from a pool of DNA populations which have been exposed to directed mutagenesis in an attempt to produce in the **library** of clones **DNA** encoding an **enzyme** having one or more desired characteristics which can be the same or different from the specified enzyme activity.

SO U.S., 10 pp., Cont.-in-part of U.S. Provisional Ser. No. 8,316, abandoned.
CODEN: USXXAM

PY 1999
1997
1997
1997
2000
1998
2000
2001
2001
2001
2002
2002
2002
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L4 ANSWER 4 OF 10 CA COPYRIGHT 2003 ACS

AB A genomic **library** of mitochondrial **DNA**, digested with EcoRI restriction **enzyme** from isolates 804001 and 804021 of Sclerotium rolfsii was constructed in the vector of pBluescript (SK+), and transformed into E. coli DH5.alpha.. Randomly selected recombinant clones designed as pSRS14, pSRS28, pSRS69, pSRS96, pSRS29, pSRS43, pSRS53 and pSRS67 were nonradioactive labeled. From dot-blot hybridization anal. with total DNA of S. rolfsii, Sclerotinia sclerotiorum and Rhizoctonia solani, the probe pSRS53 was specifically hybridized to S. rolfsii isolates. In sensitivity of the probe pSRS53 anal., it could be detected the insert DNA of pSRS53 in series up to 10-6 .mu.g and the total DNA of 804027 in series up to 10-3 .mu.g. And then the sensitivity of the probe pSRS53 to genomic DNA from internal, external scale bud of White snow and White fox, and soil exts. of lilly corms could be detected up to 10-4

.mu.g, 10-4 .mu.g, 10-4 .mu.g, 10-5 .mu.g, 10-5 .mu.g, 10-5 .mu.g, 10-5 .mu.g, resp.
SO Zhiwu Bingli Xuehuikan (1997), 6(4), 181-190
CODEN: ZBXUFM; ISSN: 1021-9544
PY 1997

L4 ANSWER 5 OF 10 CA COPYRIGHT 2003 ACS
AB Nineteen human anti-hepatitis B surface antigen (HBs) Ig clones isolated from a phage antibody **library** were analyzed with **DNA** sequencing and restriction **enzyme** mapping. They contained a single VH gene, and probably a single Vk gene also. The VH and JH gene were derived from VHIII and JHb. The D segment contained D-D fusion. Vk and Jk belonged to VkI and Jk4. Sol. Fab was expressed both in the bacterial culture supernatant and cell piroplasm. The concn. of Fab in the supernatant and cell piroplasm. The concn. of Fab in the supernatant was about 5 .mu.g/mL. The E. coli produced Fab showed specific binding to HBsAg with affinity of 0.5 .times. 109 M-1.
SO Zhonghua Weishengwuxue He Mianyixue Zazhi (1995), 15(5), 304-7
CODEN: ZWMZDP; ISSN: 0254-5101
PY 1995

L4 ANSWER 6 OF 10 CA COPYRIGHT 2003 ACS
AB A random rye genomic **library** was constructed using rye **DNA** digested with the methylation-sensitive **enzyme** Pst I. Insertions ranged from 0.5 to 2.0 kb. The low-copy clones obtained can be used as mol. genetic markers for detecting RFLPs.
SO Doklady Akademii Nauk Belarusi (1993), 37(5), 66-8
CODEN: DABSEU; ISSN: 1023-6287
PY 1993

L4 ANSWER 7 OF 10 CA COPYRIGHT 2003 ACS
AB The gene encoding the enzyme gluconolactonase (D-glucono-.delta.-lactone lactonohydrolase, EC 3.1.1.17) has been isolated from a recombinant **library** of genomic Zymomonas mobilis **DNA**, by detection of **enzyme** activity in recombinant clones. The gene encoded a protein of 320 amino acids, which is processed to the mature enzyme of 285 amino acids (31 079 Da) by cleavage at an Ala-Ala bond, as detd. from N-terminal sequencing of the purified enzyme. A minor sequence commencing at amino acid 6 is suggestive of an alternative start of translation at the ATG codon of amino acid 5; in this case the expressed enzyme would remain cytoplasmic, whereas it is presumed that the main portion is directed to the membrane or periplasm by the leader sequence.
SO Biochimica et Biophysica Acta (1992), 1171(2), 198-200
CODEN: BBACAQ; ISSN: 0006-3002
PY 1992

L4 ANSWER 8 OF 10 CA COPYRIGHT 2003 ACS
AB The distribution of d(CT)-rich pyrimidine tracts in the karyotypes of a variety of vertebrates was studied by in situ hybridization. The probe for these studies was a 56-bp homopyrimidine/homopurine sequence obtained from a mouse genomic **library** constructed with **DNA** prepd. from a restriction **enzyme** digestion of metaphase chromosomes. Single-stranded DNA nuclease digestions and 2-dimensional gel anal. of topoisomers of this sequence indicated that it is capable of adopting a triplex conformation in vitro. In situ hybridization with this probe to the karyotypes of 10 different vertebrate species revealed a highly conserved chromosomal distribution of d(CT)-rich tracts. These tracts are found throughout the chromosomal arms and in some karyotypes they are clustered, producing a banding pattern. However, at the resoln. of the light microscope, these tracts appeared to be absent from the centromeric regions of all chromosomes examd. except those of chicken. The non-random distribution of these tracts to the chromosomal arm regions implies an organizational or functional role for this repeat class. It is unlikely that the 56-bp sequence type contributed to the formation of the

triplex DNA structure previously detected in centrometric domains of mouse.
SO Chromosoma (1990), 99(5), 344-51
CODEN: CHROAU; ISSN: 0009-5915
PY 1990

L4 ANSWER 9 OF 10 MEDLINE
AB The gene encoding the enzyme gluconolactonase (D-glucono-delta-lactone lactonohydrolase, EC 3.1.1.17) has been isolated from a recombinant **library** of genomic Zymomonas mobilis **DNA**, by detection of **enzyme** activity in recombinant clones. The gene encoded a protein of 320 amino acids, which is processed to the mature enzyme of 285 amino acids (31079 Da) by cleavage at an Ala-Ala bond, as determined from N-terminal sequencing of the purified enzyme. A minor sequence commencing at amino acid 6 is suggestive of an alternative start of translation at the ATG codon of amino acid 5; in this case the expressed enzyme would remain cytoplasmic, whereas it is presumed that the main portion is directed to the membrane of periplasm by the leader sequence.
SO BIOCHIMICA ET BIOPHYSICA ACTA, (1992 Dec 29) 1171 (2) 198-200.
Journal code: 0217513. ISSN: 0006-3002.
PY 1992

L4 ANSWER 10 OF 10 MEDLINE
AB The distribution of d(CT)-rich pyrimidine tracts in the karyotypes of a variety of vertebrates was studied by in situ hybridization. The probe for these studies was a 56bp homopyrimidine/homopurine sequence obtained from a mouse genomic **library** constructed with **DNA** prepared from a restriction **enzyme** digestion of metaphase chromosomes. Single-stranded DNA nuclease digestions and two-dimensional gel analysis of topoisomers of this sequence indicated that it is capable of adopting a triplex conformation in vitro. In situ hybridization with this probe to the karyotypes of ten different vertebrate species revealed a highly conserved chromosomal distribution of d(CT)-rich tracts. These tracts are found throughout the chromosomal arms and in some karyotypes they are clustered, producing a banding pattern. However, at the resolution of the light microscope these tracts appeared to be absent from the centromeric regions of all chromosomes examined except those of chicken. The non-random distribution of these tracts to the chromosomal arm regions implies an organizational or functional role for this repeat class. It is unlikely that the 56 bp sequence type contributed to the formation of the triplex DNA structure previously detected in centromeric domains of mouse.
SO CHROMOSOMA, (1990 Sep) 99 (5) 344-51.
Journal code: 2985138R. ISSN: 0009-5915.
PY 1990

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L3 0 S LIBRARY(5W)(GENES OR DNA)(5W)DIVER?(5W)(PROTEIN(2W)VARIANT OR
L4 10 S LIBRARY(5W)(GENES OR DNA)(5W)(PROTEIN(2W)VARIANT OR ENZYME)

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L4 ANSWER 3 OF 10 CA COPYRIGHT 2003 ACS
ACCESSION NUMBER: 131:141753 CA
TITLE: Production of enzymes having desired activities by mutagenesis
INVENTOR(S): Short, Jay M.
PATENT ASSIGNEE(S): Diversa Corporation, USA
SOURCE: U.S., 10 pp., Cont.-in-part of U.S. Provisional Ser. No. 8,316, abandoned.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 24
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5939250	A	19990817	US 1996-651568	19960522
CA 2239686	AA	19970612	CA 1996-2239686	19961206
WO 9720918	A1	19970612	WO 1996-US19457	19961206
W: AU, CA, IL, JP				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9711489	A1	19970627	AU 1997-11489	19961206
AU 720334	B2	20000525		
EP 866853	A1	19980930	EP 1996-942920	19961206
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JP 2001078786	A2	20010327	JP 2000-239967	19961206
EP 1130090	A2	20010905	EP 2001-102857	19961206
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US 6171820	B1	20010109	US 1999-246178	19990204

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     US 2002068340       A1    20020606        US 1999-401861    19990922
     US 6358709          B1    20020319        US 2000-522289    20000309
     US 6361974          B1    20020326        US 2000-535754    20000327
     US 2002086279       A1    20020704        US 2001-875412    20010606
     US 2002164580       A1    20021107        US 2002-95246     20020311
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                                          US 1996-692002    A   19960802
                                          US 1996-760489    A2  19961205
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                                          JP 1997-521457    A3  19961206
                                          WO 1996-US19457   W   19961206
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                                          US 1997-988224    A1  19971210
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                                          US 2000-498557    A2  20000204
                                          US 2000-522289    A2  20000309
                                          US 2000-663620    A3  20000915
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L2             0 S LIBRARY(5W)(GENES OR DNA)(5W)DIVER?(5W)ANTIGEN
L3             0 S LIBRARY(5W)(GENES OR DNA)(5W)DIVER?(5W)(PROTEIN(2W)VARIANT OR
L4            10 S LIBRARY(5W)(GENES OR DNA)(5W)(PROTEIN(2W)VARIANT OR ENZYME)
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